

=> d his

(FILE 'HOME' ENTERED AT 16:50:17 ON 10 FEB 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE' ENTERED AT 16:50:34 ON 10 FEB 2006
L1 288 S STEROID (W) OXIDOREDUCTASE
L2 0 S L1 (A) ANTIBOD?
L3 5 S L1 AND ANTIBOD?
L4 5 DUP REM L3 (0 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 16:56:29 ON 10 FEB 2006

FILE 'REGISTRY' ENTERED AT 16:58:14 ON 10 FEB 2006
L5 1 S 9055-07-6/RN
SET NOTICE 1 DISPLAY
SET NOTICE LOGIN DISPLAY

FILE 'REGISTRY' ENTERED AT 17:01:54 ON 10 FEB 2006
L6 1 S 9044-85-3/RN
SET NOTICE 1 DISPLAY
SET NOTICE LOGIN DISPLAY
L7 2 S PROGESTERONE REDUCTASE

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE' ENTERED AT 17:04:15 ON 10 FEB 2006
L8 336 S PROGESTERONE REDUCTASE
L9 21 S L8 AND ANTIBOD?
L10 21 DUP REM L9 (0 DUPLICATES REMOVED)
L11 0 S L8 (A) ANTIBOD?
L12 0 S L8 (S) ANTIBOD?
L13 0 S L8 (P) ANTIBOD?

RESULT 3
US-09-634-955B-8
; Sequence 8, Application US/09634955B
; Patent No. 6511834
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Cook, William James
; TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
; TITLE OF INVENTION: MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-134
; CURRENT APPLICATION NUMBER: US/09/634,955B
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 69/192,002
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 8
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-634-955B-8

Query Match 97.9%; Score 1664; DB 2; Length 369;
Best Local Similarity 85.9%; Pred. No. 1.4e-183;
Matches 317; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

Qy	1 MADSAQAQKLVYLVTGGCGFLGEHVRMLLQREPRILGELRVPDQHLGPWLSELKTT----- 55
Db	1 MADSAQAQKLVYLVTGGCGFLGEHVRMLLQREPRILGELRVPDQHLGPWLSELKTGPVRV 60
Qy	56 -----GTRNVIEACVQTG 68
Db	61 TAIQGDVTQAHEVAAAAGAHVVIHTAGLVDVFGRASPPTIHEVNQGTRNVIEACVQTG 120
Qy	69 TRFLVYTSSMEVVGPNTKGHPFYRGNEDTPYEAHRHPYPCSKALAEWLVLBANGRKVRG 128
Db	121 TRFLVYTSSMEVVGPNTKGHPFYRGNEDTPYEAHRHPYPCSKALAEWLVLBANGRKVRG 180
Qy	129 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAlPASVEHGRVYVGNVAVMHVL 188
Db	181 GLPLVTCALRPTGIYGEGHQIMRDFYRQGLRLGGWLFRAlPASVEHGRVYVGNVAVMHVL 240
Qy	189 AARELQRAALMGGQVYFCYDGSPYRSYEDFNMEFLGPCGLRLVGARPLLPYWLVLFLAA 248
Db	241 AARELQRAALMGGQVYFCYDGSPYRSYEDFNMEFLGPCGLRLVGARPLLPYWLVLFLAA 300
Qy	249 LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 308
Db	301 LNALLQWLLRPLVLYAPLLNPYTLAVANTTFTVSTDKAQRHFGYEPLFSWEDSRTRTILW 360
Qy	309 VQAATGSAQ 317
Db	361 VQAATGSAQ 369